Amendments to the Claims:

The following listing of claims will replace all prior versions, and listings, of claims in the application:

1. (Previously Presented) A method for assaying the presence or the absence of at least one mutation on a strand of nucleic acids paired in a duplex form, comprising:

contacting in a liquid medium said duplex, suspected to include at least one mismatch with at least one compound able to undergo a specific base pairing interaction with said mismatch, said compound(s) being used at a combined concentration of at least 10g/l in said medium; and

assaying for said mismatch by an analytical method.

2. (Original) The method according to claim 1, wherein the strands of nucleic acids paired in duplex form are two DNA strands which are in all or in part complementary.

3. (Previously Presented) A method for performing Electrophoretic Heteroduplex Analysis "EHDA" on a nucleic acid sample suspected to include at least one heteroduplex, comprising:

contacting in a liquid medium said nucleic acid sample suspected to include at least one heteroduplex, with at least one compound able to undergo a specific base pairing interaction with at least one mismatch of said heteroduplex, said compound(s) being used at a combined concentration of at least 10g/l of said medium,

assaying for the presence of said heteroduplex thanks to its electrophoretic mobility.

4. (Original) The method according to claim 3 comprising a preliminary step of denaturating the nucleic acid sample and renaturating it in conditions convenient to achieve both heteroduplexes and homoduplexes.

5. (Previously Presented) A method for assaying the presence or the absence of at least one mutation on a single strand of nucleic acid in a liquid medium, comprising:

(a) contacting said nucleic acid suspected to include at least one mutation with a nucleic acid probe grafted on a solid support,

(b) allowing the hybridization of at least a part of said strand of nucleic acid with the grafted nucleic acid probe,

(c) washing non-hybridized strands, and

(d) assaying for said mutation by an analytical method,

wherein the steps a) and/or c) are performed in the presence of at least one compound able to undergo a specific base pairing interaction with said mutation, said compound being at a concentration of at least lg/l.

6. (Previously Presented) The method according to claim 1 wherein the strand(s) of nucleic acids is a single stranded DNA, RNA, LNA, PNA, or any artificial or natural analog of nucleic acids.

7. (Previously Presented) The method according to claim 1, wherein the compound able to undergo a specific base pairing interaction includes at least two groups suitable for hydrogen bonding, in an orientation, polarity and spacing compatible with the creation of attractive interaction with at least one of the bases A, T, G, C and U.

8. (Previously Presented) The method according to claim 1, wherein said compound is unable to interfere with polymerisation reactions of nucleotides and/or to be incorporated into a newly polymerized DNA strand.

9. (Previously Presented) The method according to claim 1, wherein said compound is one oligonucleotide having a length of less than 5 nucleotides, a nucleoside, a base or a mixture thereof.

10. (Previously Presented) The method according to claim 9, wherein the oligonucleotide has a length of less than 3 nucleotides.

11. (Previously Presented) The method according to claim 9, wherein the compound is selected among adenosine, guanosine, uridine, cytidine, thymidine and mixtures thereof.

12. (Previously Presented) The method according to claim 9, wherein oligonucleotide(s) or nucleoside(s) in the mixture of oligonucleotides or nucleosides are unable to undergo mutually base pairing interaction.

13. (Original) The method according to claim 12, wherein the compound includes cytidine and thymidine or cytidine and adenosine or guanosine and thymidine or guanosine and adenosine.

14. (Previously Presented) The method according to claim 1, wherein the compound(s) is used at a concentration of at least 25 g/l.

15. (Previously Presented) The method according to claim 1, in which said compound(s) is in addition bearing at least one substituent.

16. (Previously Presented) The method according to claim 15, in which said substituent induces in said compound at least one of the following changes:

increase in solubility,

change in charge, or

change in friction with a solvent.

17. (Previously Presented) The method according to claim 1, wherein the mutation to assay is a point mutation.

18. (Previously Presented) The method according to claim 1, wherein said mutation is assayed by hybridization assay.

19. (Previously Presented) The method according to claim 1, wherein said mutation is assayed by an electrophoretic analysis using a liquid separating medium.

20. (Previously Presented) The method according to claim 19, wherein said liquid separating medium contains at least a polymer at a concentration of at least 1% by weight of the total weight of said medium.

21. (Previously Presented) The method according to claim 19, wherein said liquid separating medium contains at least a polymer chosen from the group consisting of N,N-disubstituted polyacrylamides and N- substituted polyacrylamides, wherein said N substituents are selected from the group consisting of C_1 to C_{12} alkyl, halo-substituted C_1 to C_{12} alkyl, methoxy-substituted C_1 to C_{12} alkyl, and hydroxyl-substituted C_1 to C_{12} alkyl.

22. (Previously Presented) The method according to claim 20, wherein the liquid separation medium contains at least one polymer composed of several polymer segments, said polymer being of the irregular block copolymer type or irregular comb polymer type and having on average at least three junction points established between polymer segments of different chemical or topological nature.

23. (Previously Presented) The method according to claim 22, wherein the polymer comprises at least one type of polymer segment showing, within the separating medium, specific affinity for a channel wall, and at least one type of polymer segment showing in said medium less or no affinity for said wall.

24. (Previously Presented) The method according to claim 20, wherein said polymer contains acrylamide or substituted acrylamides.

25. (Currently Amended) A method for diagnosing a predisposition to genetic diseases or cancers associated or putatively associated to specific point mutation(s) or the diagnosis or prognosis of said diseases or cancers, comprising:

contacting in a liquid medium said duplex, suspected to include at least one mismatch with at least one compound able to undergo a specific base pairing interaction with

said mismatch, said compound(s) being used at a combined concentration of at least ~~1g/l~~ 10g/l in said medium; and

assaying for said mismatch by an analytical method.

26. (Previously Presented) The method according to claim 25, wherein said disease is associated to at least a point mutation in a human breast cancer predisposition gene (BRCA).

27. (Original) A composition including at least a compound able to undergo specific base pairing interaction at a concentration of at least 1 g/l and at least a liquid separating medium.

28. (Previously Presented) The composition according to claim 27, wherein the compound able to undergo a specific base pairing interaction includes at least two groups suitable for hydrogen bonding, in an orientation, polarity and spacing compatible with the creation of attractive interaction with at least one of the bases A, T, G, C and U.

29. (Canceled).

30. (Previously Presented) The composition according to claim 27, wherein said liquid separation medium includes furthermore at least a compound selected among:

a sieving polymer

a hydrophilic polymer, and

a surface-active polymer.

31. (Previously Presented) A composition including at least a DNA fragment having a nucleic sequence related to a gene on which point mutation(s) has been associated or putatively associated with a disease or an increased predisposition to a disease, and at least a compound able to undergo specific base pairing interaction, said compound(s) being used at a concentration of at least 10g/l, wherein said compound able to undergo a specific base pairing interaction includes at least two groups suitable for hydrogen bonding, in an orientation,

polarity and spacing compatible with the creation of attractive interaction with at least one of the bases A, T, G, C and U.

32. (Previously Presented) A composition including at least a compound able to undergo specific base pairing interaction at a concentration of at least lg/l, and a pair of DNA probes, wherein said compound able to undergo a specific base pairing interaction includes at least two groups suitable for hydrogen bonding, in an orientation, polarity and spacing compatible with the creation of attractive interaction with at least one of the bases A, T, G, C and U.

33. (Previously Presented) A kit useful for the screening of a nucleic acid or analog thereof having a sequence related to a gene on which point mutation(s) has been associated or putatively associated with a disease or an increased predisposition to a disease, said kit comprising at least a composition according to claim 27.

34. (Previously Presented) A method for assaying a nucleic acid for mutation, comprising:

performing a polymerase chain reaction on said nucleic acid in the presence of at least two primers and a pool of compounds able to undergo specific base pairing interaction with nucleotides or analogue thereof, said compounds being at a combined concentration of at least 1 g/l and being unable to interfere with the polymerase chain reaction; and

analyzing and/or quantifying the so-obtained DNA fragments.

35. (Previously Presented) The method according to claim 34, wherein the compound able to undergo a specific base pairing interaction includes at least two groups suitable for hydrogen bonding, in an orientation, polarity and spacing compatible with the creation of attractive interaction with at least one of the bases A, T, G, C and U.